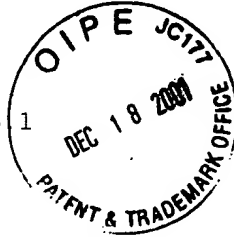


4

032301.205.seq.ST25.txt
SEQUENCE LISTING

<110> BATHE, Brigitte
<120> NUCLEOTIDE SEQUENCES WHICH CODE FOR THE sigH GENE
<130> 032301 WD 295
<160> 4
<170> PatentIn version 3.1
<210> 1
<211> 1148
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (302)..(919)
<223>



<400> 1
ttgttgatgg ctgtggctaa atcatcgta tctttggggc gtaatcgatg ccaaaatgcg 60
aggtcacggc gattagtctc aacaatttcg gtgcttaaag gatcctgcgg attattgacg 120
gtgaagtaga acattgtttc cccctagatt tgaagtggta catatgttct aactgatgtg 180
gtggacacgc gggggtagag taaagtctaa gcaacagctc acgtggcttt acagctaccc 240
ccgaaaggtc tgttttttat cggaagtaga atagtcaaca cgcattttcg aaaggggcc 300
c atg gct gaa aac cga acc ggc aca gtc gat gga gac gcg ttg gct gcc 349
Met Ala Glu Asn Arg Thr Gly Thr Val Asp Gly Asp Ala Leu Ala Ala
1 5 10 15
cgc ttt gaa gag gag gca ctg cca ctc ctt gac cag ctc tat ggc ggt 397
Arg Phe Glu Glu Glu Ala Leu Pro Leu Leu Asp Gln Leu Tyr Gly Gly
20 25 30
gct ctg cgc atg act aga aat ccc gca gat gcg gaa gat ctc gtg caa 445
Ala Leu Arg Met Thr Arg Asn Pro Ala Asp Ala Glu Asp Leu Val Gln
35 40 45
gac acc tat atc aag gcg tac cag gcg ttc gcg agc ttc aaa cca ggc 493
Asp Thr Tyr Ile Lys Ala Tyr Gln Ala Phe Ala Ser Phe Lys Pro Gly
50 55 60
acc aac ctg aag gct tgg ctc tat cgg atc atg acg aat acc tac atc 541
Thr Asn Leu Lys Ala Trp Leu Tyr Arg Ile Met Thr Asn Thr Tyr Ile
65 70 75 80
aac atg tac cga aag aaa cag agg cag cca tcg caa acc tct gcc gat 589
Asn Met Tyr Arg Lys Lys Gln Arg Gln Pro Ser Gln Thr Ser Ala Asp
85 90 95
gag atc act gac tac cag ctc gtt gaa tct caa tcg cat acc tca aca 637

032301.205.seq.ST25.txt

Glu Ile Thr Asp Tyr Gln Leu Val Glu Ser Gln Ser His Thr Ser Thr
 100 105 110
 ggg ctg gaa tcc gcc gag gtt gag gct ctg aaa aat ctg cca gac gga 685
 Gly Leu Glu Ser Ala Glu Val Glu Ala Leu Lys Asn Leu Pro Asp Gly
 115 120 125
 aaa att ggc gat gca atg aat caa ctc agc ccg gaa tac cgg atg gtg 733
 Lys Ile Gly Asp Ala Met Asn Gln Leu Ser Pro Glu Tyr Arg Met Val
 130 135 140
 gtt tat tat gcc gat gta gaa gat ctc gca tac aaa gaa atc gcc gag 781
 Val Tyr Tyr Ala Asp Val Glu Asp Leu Ala Tyr Lys Glu Ile Ala Glu
 145 150 155 160
 atc atg gac gtt cca ctc gga act gtg atg tcc cga ctc cat cgt gga 829
 Ile Met Asp Val Pro Leu Gly Thr Val Met Ser Arg Leu His Arg Gly
 165 170 175
 aga aaa cag ctc cga gga atg tta aag gaa gta gcg aag gaa caa ggc 877
 Arg Lys Gln Leu Arg Gly Met Leu Lys Glu Val Ala Lys Glu Gln Gly
 180 185 190
 att ggt ctt gaa cat ccc gac atg aag aaa aat tcg gag gca 919
 Ile Gly Leu Glu His Pro Asp Met Lys Lys Asn Ser Glu Ala
 195 200 205
 taacgatgac gaatctcaac cgcagcgcact cgcaaggtga ttgtggctgc cctgaattct 979
 tcgatgaaat gtatcagcta ctgcacgata aactcagcga gtccgcctgc gagcgtctgc 1039
 ggattcacgc ggcaggctgc ccggcatgcc agcaactgct agaggccgaa tcggagtttc 1099
 gtagtctgtt gcgcaagtgc tgctgcgaat cggcacctgt ggagctccg 1148

 <210> 2
 <211> 206
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 2
 Met Ala Glu Asn Arg Thr Gly Thr Val Asp Gly Asp Ala Leu Ala Ala
 1 5 10 15
 Arg Phe Glu Glu Glu Ala Leu Pro Leu Leu Asp Gln Leu Tyr Gly Gly
 20 25 30
 Ala Leu Arg Met Thr Arg Asn Pro Ala Asp Ala Glu Asp Leu Val Gln
 35 40 45
 Asp Thr Tyr Ile Lys Ala Tyr Gln Ala Phe Ala Ser Phe Lys Pro Gly
 50 55 60

032301.205.seq.ST25.txt

Thr Asn Leu Lys Ala Trp Leu Tyr Arg Ile Met Thr Asn Thr Tyr Ile
65 70 75 80

Asn Met Tyr Arg Lys Lys Gln Arg Gln Pro Ser Gln Thr Ser Ala Asp
85 90 95

Glu Ile Thr Asp Tyr Gln Leu Val Glu Ser Gln Ser His Thr Ser Thr
100 105 110

Gly Leu Glu Ser Ala Glu Val Glu Ala Leu Lys Asn Leu Pro Asp Gly
115 120 125

Lys Ile Gly Asp Ala Met Asn Gln Leu Ser Pro Glu Tyr Arg Met Val
130 135 140

Val Tyr Tyr Ala Asp Val Glu Asp Leu Ala Tyr Lys Glu Ile Ala Glu
145 150 155 160

Ile Met Asp Val Pro Leu Gly Thr Val Met Ser Arg Leu His Arg Gly
165 170 175

Arg Lys Gln Leu Arg Gly Met Leu Lys Glu Val Ala Lys Glu Gln Gly
180 185 190

Ile Gly Leu Glu His Pro Asp Met Lys Lys Asn Ser Glu Ala
195 200 205

<210> 3
<211> 28
<212> DNA
<213> Corynebacterium glutamicum

<400> 3
caggtacctt ttcgaaaggg gccacatg 28

<210> 4
<211> 28
<212> DNA
<213> Corynebacterium glutamicum

<400> 4
tgtctagaaa gaattcaggg cagccaca 28